



Title: 15625 Receptor, A Novel G-Protein
Coupled Receptor
Inventor(s): Glucksmann et al.
Application No: Not Assigned
Atty Dkt No: 35800/238853(5800-13B)

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Input file flh15625cons; Output File 15625tr
Sequence length 2286

CGTCCGTAGCTTTGAGTCCAGTGTTTGAAGACAATCTCTGATTGTGAAGCCCTCTTTTCTCTCCTTCTATTCTCTCT
AGAGCACTCAAGACTTTACTGACGAAACTCAGGAAATCCTCTATCACAAGAGGTTTGGCAACTAAACTAAGACATTA
AAAGGAAAATACCAGATGCCACTCTGCAGGCTGCAATAACTACTACTTACTGGATACATTCAAACCTCCAGAATCAAC

M Q A V D N L T S A P G N T 14
AGTTATCAGGTAACCAACAAGAA ATG CAA GCC GTC GAC AAC CTC ACC TCT GCG CCT GGG AAC ACC 42

S L C T R D Y K I T Q V L F P L L Y T V 34
AGT CTG TGC ACC AGA GAC TAC AAA ATC ACC CAG GTC CTC TTC CCA CTG CTC TAC ACT GTC 102

L F F V G L I T N G L A M R I F F Q I R 54
CTG TTT TTT GTT GGA CTT ATC ACA AAT GGC CTG GCG ATG AGG ATT TTC TTT CAA ATC CCG 162

S K S N F I I F L K N T V I S D L L M I 74
AGT AAA TCA AAC TTT ATT ATT TTT CTT AAG AAC ACA GTC ATT TCT GAT CTT CTC ATG ATT 222

L T F P F K I L S D A K L G T G P L R T 94
CTG ACT TTT CCA TTC AAA ATT CTT AGT GAT GCC AAA CTG GGA ACA GGA CCA CTG AGA ACT 282

F V C Q V T S V I F Y F T M Y I S I S F 114
TTT GTG TGT CAA GTT ACC TCC GTC ATA TTT TAT TTC ACA ATG TAT ATC AGT ATT TCA TTC 342

L G L I T I D R Y Q K T T R P F K T S N 134
CTG GGA CTG ATA ACT ATC GAT CGC TAC CAG AAG ACC ACC AGG CCA TTT AAA ACA TCC AAC 402

P K N L L G A K I L S V V I W A F M F L 154
CCC AAA AAT CTC TTG GGG GCT AAG ATT CTC TCT GTT GTC ATC TGG GCA TTC ATG TTC TTA 462

L S L P N M I L T N R Q P R D K N V K K 174
CTC TCT TTG CCT AAC ATG ATT CTG ACC AAC AGG CAG CCG AGA GAC AAG AAT GTG AAG AAA 522

C S F L K S E F G L V W H E I V N Y I C 194
TGC TCT TTC CTT AAA TCA GAG TTC GGT CTA GTC TGG CAT GAA ATA GTA AAT TAC ATC TGT 582

Q V I F W I N F L I V I V C Y T L I T K 214
CAA GTC ATT TTC TGG ATT AAT TTC TTA ATT GTT ATT GTA TGT TAT ACA CTC ATT ACA AAA 642

E L Y R S Y V R T R G V G K V P R K K V 234
GAA CTG TAC CGG TCA TAC GTA AGA ACG AGG GGT GTA GGT AAA GTC CCC AGG AAA AAG GTG 702

N V K V F I I I A V F F I C F V P F H F 254
AAC GTC AAA GTT TTC ATT ATC ATT GCT GTA TTC TTT ATT TGT TTT GTT CCT TTC CAT TTT 762

A R I P Y T L S Q T R D V F D C T A E N 274
GCC CGA ATT CCT TAC ACC CTG AGC CAA ACC CGG GAT GTC TTT GAC TGC ACT GCT GAA AAT 822

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FIG 1A



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T L F Y V K E S T L W L T S L N A C L D 294
ACT CTG TTC TAT GTG AAA GAG AGC ACT CTG TGG TTA ACT TCC TTA AAT GCA TGC CTG GAT 882

P F I Y F F L C K S F R N S L I S M L K 314
CCG TTC ATC TAT TTT TTC CTT TGC AAG TCC TTC AGA AAT TCC TTG ATA AGT ATG CTG AAG 942

C P N S A T S L S Q D N R K K E Q D G G 334
TGC CCC AAT TCT GCA ACA TCT CTG TCC CAG GAC AAT AGG AAA AAA GAA CAG GAT GGT GGT 1002

D P N E E T P M * 343
GAC CCA AAT GAA GAG ACT CCA ATG TAA 1029

ACAAATTAAGGAAATATTTCAATCTCTTTGTGTTGAGAACTCGTTAAAGCAAAGCGCTAAGTAAAAATATTAAGT
GACGAAGAAGCAACTAAGTTAATAATAATGACTCTAAAGAAACAGAAGATTACAAAAGCAATTTTCATTTACCTTTCCA
GTATGAAAAGCTATCTTAAATATAGAAAACCTAATCTAACTGTAGCTGTATTAGCAGCAAAAACAAACGACATCCAATT
GTCATGCTGCATGCAAACTACACAGAATTCATGTTTTCAGAGTTTTCGCAAAATGAGTAATCATATAATATTTACTG
TAATTTTTTAAATACATTATCGTTTCAATTTTATTTTTCATAATCAACTAAGGAAGAAGCATCAATTGGATATAATT
TCTTACCAAAATGATAGTTAAATGTATATATATCTAGTCCCTAACCAATCTGACCTATTGGGATACCTTATAAA
AATTTAAGTAAGTGGGATACACAAAGAATAAATACTATTAACCTTTTCATTATTAGCAAAAACCTAAGGGATTTAAACTA
ATTGAACTGTATTTGATTGGACTTAATTTTTTATGTTTATTTAGAAGATAAAGATTTAAAGAAGACCTTTACAATAAA
GAGAAGAAATATCGAAGTCATTAAATAAGGAGACTTACTTTTATGACATTCTAATACTAAAAATATAGAAATATTTTC
CTTAATCTAGAGAACTAGTTTTACTAATTTTTTACAACCTCAATAATACCATCACTGACACTTACCTTTATTAATTA
GCTTCTAGAAAATAGCTGCTAATTAGGTTAATGAACATTTTACCTTAGTGAAAAAATTAATTAAATATGATTACAAAG
TTGCACAGCATAACTACTGAGAGGAAAGTGATTGATCTGTTTGTAAATTACTTGTGTTGTATGGTGTGTATAAAATACAA
AATTTACATTAAGCTCTAAAAAAGGGCGG

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FIG 1B



Title: 15625 Receptor, A Novel G-Protein
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Atty Dkt No: 35800/238853(5800-13B)

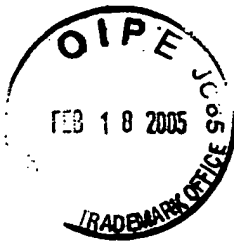
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```
>PF00001|PF00001 7 transmembrane receptor (rhodopsin family)
Score: 184.21 Seq: 42 298 Model: 1 269
*GNiLVlWvIcRyRRMRTPMNYFivNLAvADLLFslftMPFWMvYyvMgg
N+L + +++++ R+ ++ + +F+ N ++DLL+ ++T+PF +++ + G
Flh15625or 42 TNGLAMRIFFQIRS-KSNFIIFLKNTVISDLLM-ILTFPFKILSDAKLG 88
RWpFGdfmCrIWmYFDYMNMYASIFfLTcISIDRYLWAICHPMrYmRWMT
+ P+ +F+C +++ ++Y++MY SI FL +I+IDRY+ ++P++ + +
Flh15625or 89 TGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQ-KTTRPFKTSNPKN 137
pRHRawMIiiiWvMSFlISMPPFLMFrWstYrDEneWnmTWcmIyDWPe
+ A+++++IW+++FL+S+P + M+ + T+R ++ N+ C++ E
Flh15625or 138 LL-GAKILSVVIWAFMFLLSLP-N-MI-L-TNRQPRDKNVKKCSF-LKSE 181
..WMWrWYvILmtiimgFYIPMiIMlFCYwRIYRIaRlWMRMIpswQrRR
W +V ++ + F I ++I ++CY++I +++++ ++ +++ +
Flh15625or 182 FGLVWHEIVNYICQ-VIFWINFLIVIVCYTLITKELYRSYVRTRGVGK-- 228
rmSmRrERRivKMliiIMvVFIIICWlPYFivmFMDTLM.MwwFCefC.Iw
++++ ++II+ VF+IC+ P++ + + +TL ++ ++ +
Flh15625or 229 ----VPRKKVNVKFIIIAVFFICFVPFHFARIPYTLsqTRDVFdCTaEN 274
rrlWmY.IfewLaYvNCpCiNPIIY*
++++ ++WL ++N C++P+IY
Flh15625or 275 TLFYVKESTLWLTSLNA-CLDPFIY 298
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FIG 2

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Atty Dkt No: 35800/238853(5800-13B)



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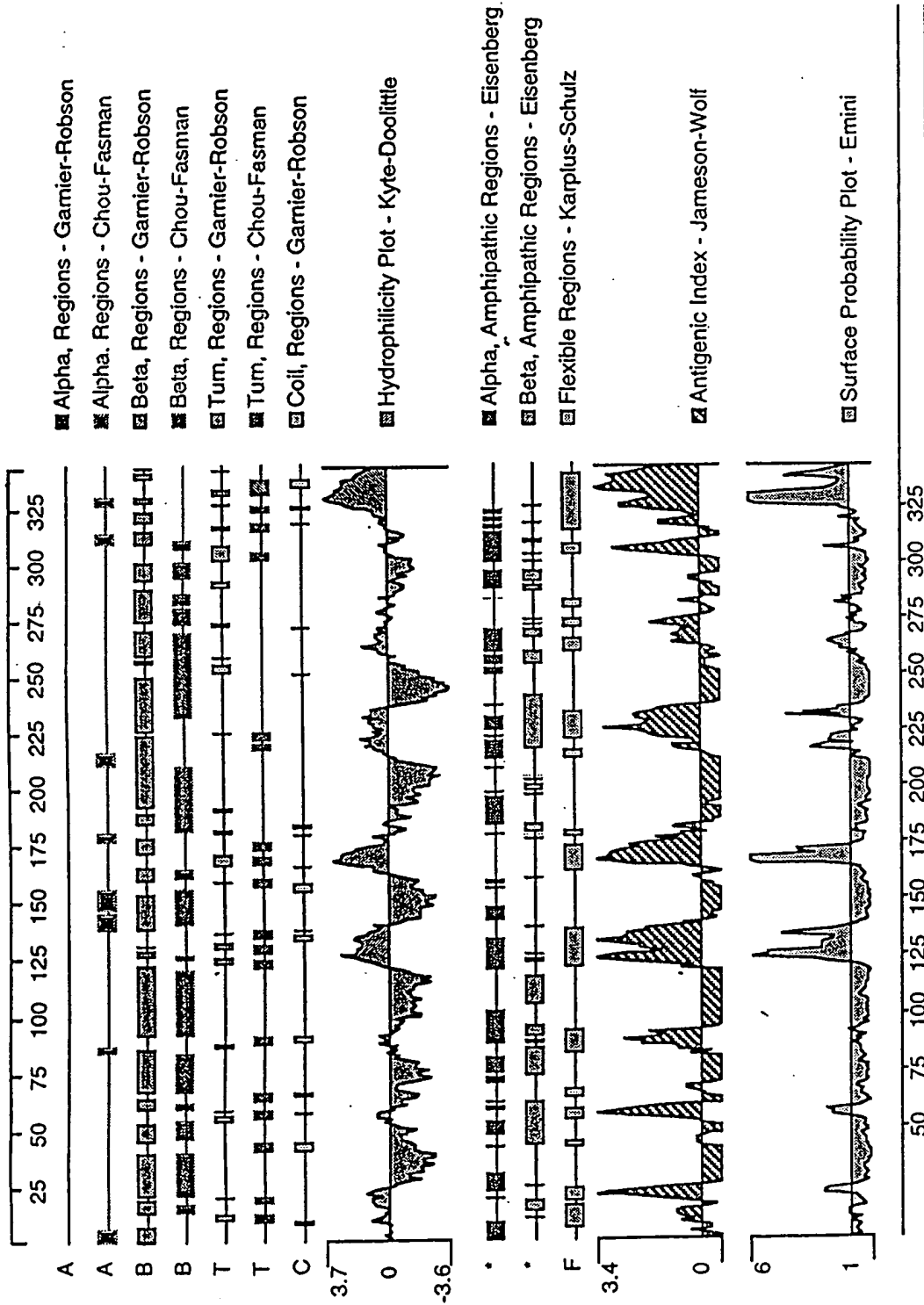
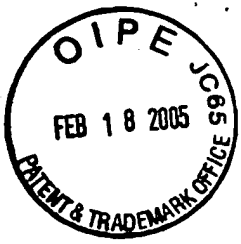


FIG 3

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15625orfaa -> KD Hydrophobicity <11/1>

Protein sequence 343 a.a. MQAVDNLTSAPG ... DGGDPNEETPMZ

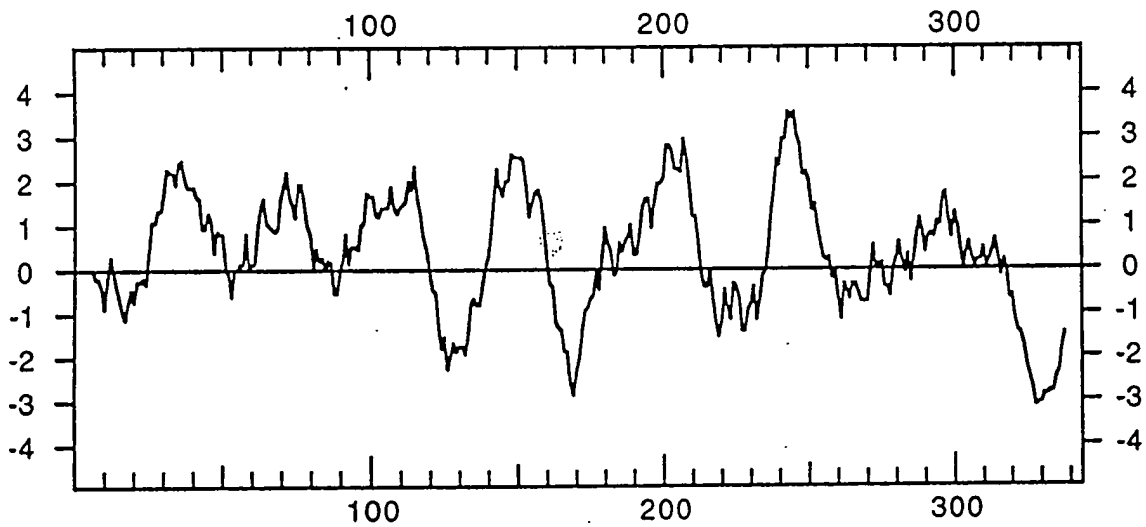


FIG 4

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>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.
N[^*P][ST][^*P]

Query: 6 nlts 9

Query: 13 ntst 16

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase
phosphorylation site.
[RK](2)[A-Z][ST]

Query: 173 kkcs 176

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.
[ST][A-Z][RK]

Query: 126 ttr 128

Query: 163 tnr 165

Query: 304 sfr 306

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.
G[^*EDRKHPFYW][A-Z](2)[STAGCN][^*P]

Query: 39 glitng 44

Query: 333 ggd pne 338

FIG 5



Title: 15625 Receptor, A Novel G-Protein
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Input file 79a2cons; Output File 79a2tra
Sequence length 2272

ACGCGTCCGCAATCTCTGATTGTAAAGCCCTCTCTTCCTCTCCTTCTATTTCTCTATAGAACACTCAAGACTTTACTGA
TGAAAACCTCAGGAAATTCTCTATCACAAAGAGGTTTGGCAACTAACTAAGACATTAAAAGGAAAATACCAGATGCCAC
TCTGCACGTTGCAATAACTACTATTCTGATACATTCAAATCCTCCAGAATCAACGGTTATCAGGTAACCAACAAGA

M Q A I D N L T S A P G N T S L C T R	19
A ATG CAA GCC ATC GAC AAC CTC ACG TCT GCG CCT GGG AAC ACC AGT CTG TGC ACC AGA	57
D Y K I T Q V L F P L L Y T V L F F V G	39
GAC TAC AAA ATC ACC CAG GTC CTC TTC CCA CTG CTC TAC ACT GTC CTG TTT TTT GTT GGA	117
L I T N S L A M R I F F Q I R S K S N F	59
CTC ATC ACA AAT AGC CTG GCG ATG AGG ATT TTC TTT CAA ATT CGG AGT AAA TCA AAC TTT	177
I I F L K N T V I S D L L M I L T F P F	79
ATT ATT TTT CTT AAG AAC ACA GTC ATT TCC GAT CTT CTC ATG ATT CTG ACT TTT CCA TTC	237
K I L S D A K L G T G P L R T F V C Q V	99
AAA ATT CTT AGT GAT GCC AAA CTG GGA ACA GGA CCA CTG AGA ACT TTT GTG TGT CAA GTT	297
T S V I F Y F T M Y I S I S F L G L I T	119
ACC TCC GTC ATA TTT TAT TTC ACA ATG TAT ATC AGT ATT TCA TTC CTG GGA CTG ATA ACT	357
I D R Y Q K T T R P F K T S N P K N L L	139
ATC GAT CGC TAC CAG AAG ACC ACC AGG CCA TTT AAA ACA TCC AAC CCC AAA AAT CTC TTG	417
G A K I L S V L I W A F M F L L S L P N	159
GGG GCT AAG ATT CTC TCT GTT CTC ATC TGG GCA TTC ATG TTC TTA CTC TCT TTG CCT AAC	477
M I L T N R R P R D K N V K K C S F L K	179
ATG ATT CTG ACT AAC AGG CGG CCA AGA GAC AAG AAT GTG AAG AAA TGC TCT TTC CTT AAA	537
S E F G L V W H E I V N Y I C Q V I F W	199
TCA GAG TTC GGC CTA GTC TGG CAT GAA ATA GTA AAT TAC ATC TGT CAA GTC ATT TTC TGG	597
I N F L I V I V C Y T L I T K E L Y R S	219
ATT AAT TTC TTA ATT GTC ATT GTA TGT TAC ACA CTC ATT ACA AAA GAA CTG TAC CGG TCA	657
Y V R T R G V G K V P R K K V N V K V F	239
TAT GTA AGA ACA AGG GGT GTA GGT AAA GTC CCC AGG AAA AAG GTG AAC GTC AAA GTT TTC	717
I I I A V F F I C F V P F H F A R I P Y	259
ATT ATC ATT GCT GTA TTC TTT ATT TGT TTT GTT CCT TTC CAT TTT GCC CGA ATT CCT TAT	777
T L S Q T R D V F D C A A E N T L F Y V	279
ACC CTG AGC CAA ACC CGG GAT GTC TTT GAC TGC GCC GCT GAA AAT ACT CTG TTC TAT GTG	837

FIG 6A

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K E S T L W L T S L N A C L D P F T Y F	299
AAA GAG AGT ACT CTG TGG TTA ACT TCC TTA AAT GCA TGC CTG GAT CCG TTC ACC TAT TTT	897
F L C K S F R N S L I S M L K C P N S A	319
TTC CTT TGC AAG TCC TTC AGA AAT TCC TTG ATA AGT ATG CTG AAG TGC CCC AAT TCT GCA	957
T S Q S Q D N R K K E Q D G G D P N E E	339
ACA TCT CAG TCC CAG GAC AAT AGG AAA AAA GAA CAG GAT GGT GGT GAC CCA AAT GAA GAG	1017
T P M *	343
ACT CCA ATG TAA	1029

ACATATTAAGTGAAGAAATATGTCAATCTCTTTGCGTTTCAGAACTCATTAAAGCAAAGCGCTACGTAAAAATATTAAGT
GACGAAGAAGCAACTGAGTTAATAACAATGACTCTTAAACATGTAATAGAAGATTACAAAAGCAATTTTCATTTACC
TTTCCAGTATGAAAAGCTATGTTAAATATAGAAAATAATCTAACCTGTAGCTGTATAGTATCAAAACAAATGACATC
CAATTGGCATGCTGCATGCAAACTACACAGAATTCACGTTTTGTCAGAGTTTTGCCAAAATGAGTAATCATATAATATC
TACCGTAATGTTTAAATACATTATTGCTCAGGATTTTATTTCTTCATAATCAACTAAGGAAGAATTATCAATTGGATA
CAATCTTCTTACAAAAAATGACACTTAAATGTATATATATCCTAGCCCCTAACCAATCCTGACCTATTGGGATACTT
ATAAAATTTGAGTAAGTGGGATACACAAAGAATAATAACTATTAAGTTTTAAATTATGAGCAAAACCTAAGGGTTAAA
TTTAACTAATTGAACTGTATTTGATTGGACTTAATTTTTTTGTTTATTAAGAAGACACTTGAAGAAGACCTTTACAA
TAAAGAGAAGAAATATCAAAGTCATTAAATAAGGAGAGTTACTTTTATGATATTCTAACACTAAACAATATAGAAATA
TTTCCTTAATATTAGTTTCTAGAGAACTAGTTTACTAATTTTTTACAACCTCAATAATACCATCATTGACACTTACC
TTTATTAAGTCTCTAGAAAATACCTGCTAATTAGGTTAATGAACATTTTATGTTAGTGAAAAAATTAATTAAATA
TGATTACAAAGTTGCACAGCATAACTACTGAAAGTGATTGATCCATTTGTAATTATTTGTTGTACTGGTGTGTATAAA
ATACAAAATTTACATTAACTCTAAATCACCAAAAAAAAAAAAAAAAAAAGGGCGG

FIG 6B

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